FIGURE 1

Monkey #6 (Intranodal Administration)
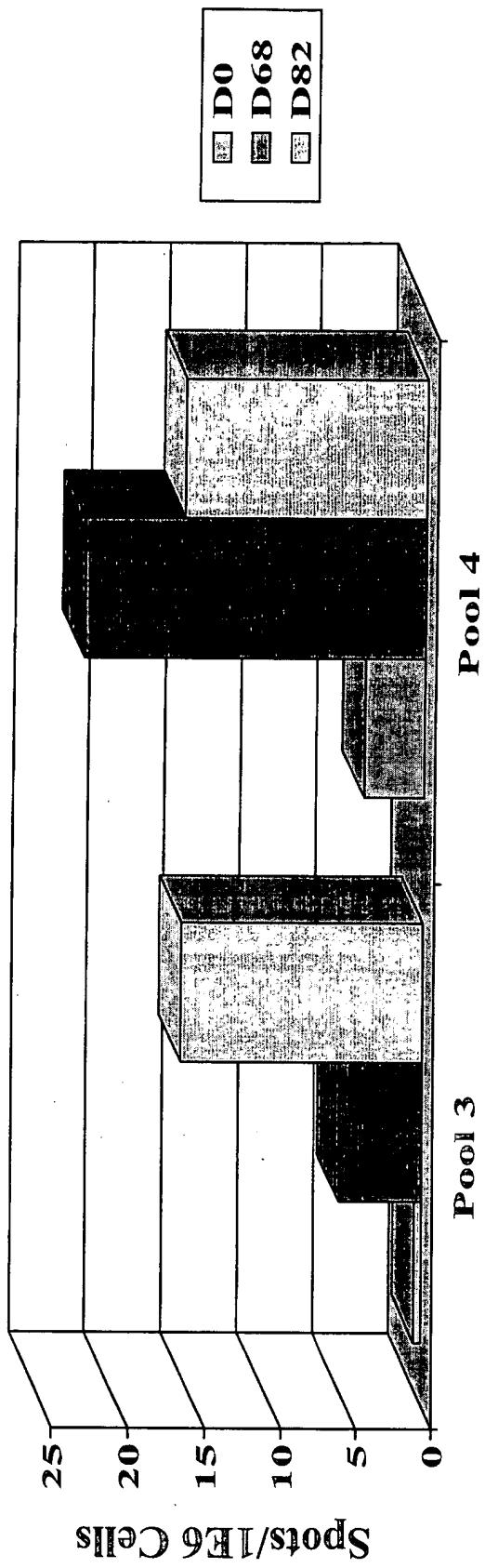
FIGURE 2

Monkey #7 (Intranodal Administration)

Legend: D0, D68, D82
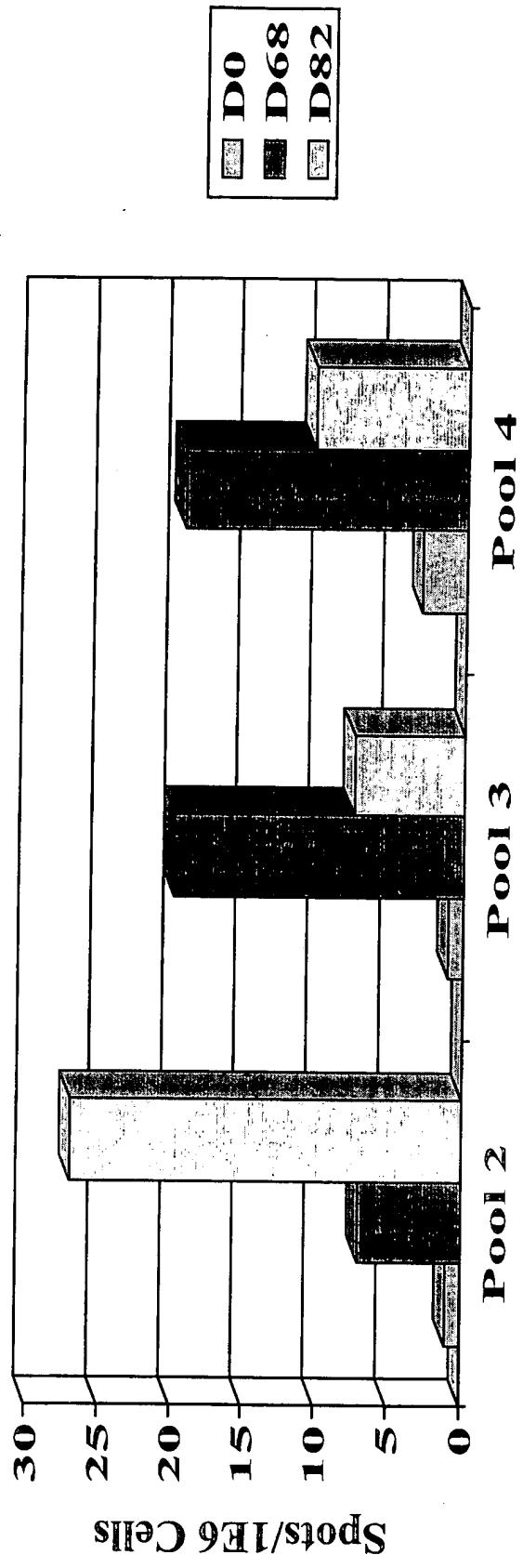
FIGURE 3

Monkey # 11 (Subcutaneous Administration)

Legend:
- D0
- D68
- D82

Y-axis: Spots/1E6 Cells (values: 0, 5, 10, 15, 20, 25, 30)

X-axis: Pool 4
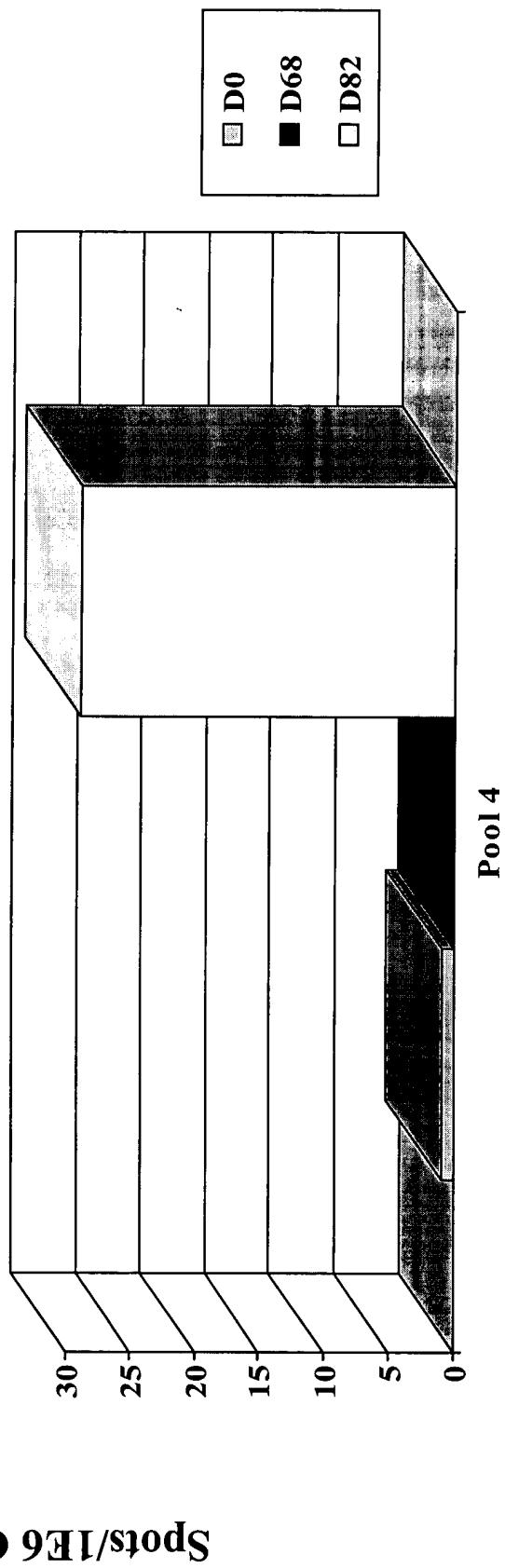
FIGURE 4

Monkey #10 (Subcutaneous Administration)

FIGURE 5

Antibodies to gp100

Kinetics ELISA mOD/min vs Day of bleed

CONTROL
subcutaneous
INTRANODAL
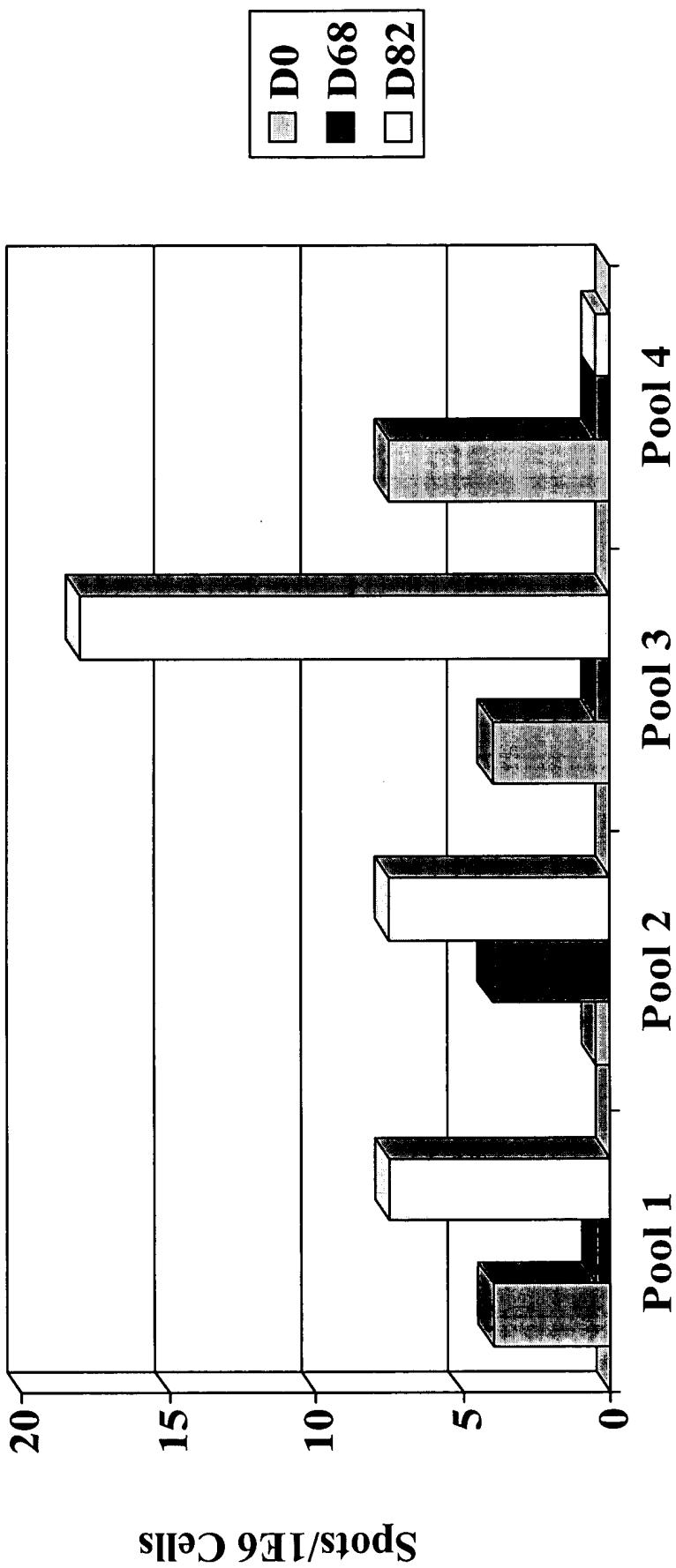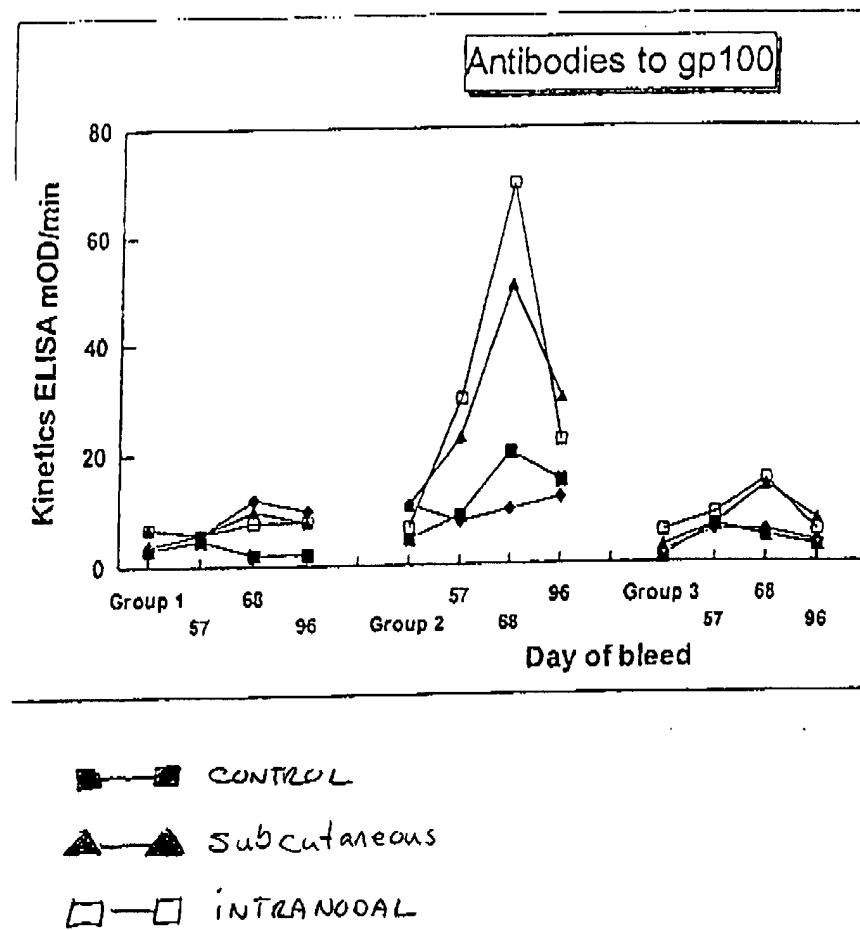
FIGURE 6

```
                              ATGG ATCTGGTGCT AAAAAGATGC CTTCTTCATT TGGCTGTGAT
AGGTGCTTTG CTGGCTGTGG GGGCTACAAA AGTACCCAGA AACCAGGACT GGCTTGGTGT
CTCAAGGCAA CTCAGAACCA AAGCCTGGAA CAGGCAGCTG TATCCAGAGT GGACAGAAGC
CCAGAGACTT GACTGCTGGA GAGGTGGTCA AGTGTCCCTC AAGGTCAGTA ATGATGGGCC
TACACTGATT GGTGCAAATG CCTCCTTCTC TATTGCCTTG AACTTCCCTG GAAGCCAAAA
GGTATTGCCA GATGGGCAGG TTATCTGGGT CAACAATACC ATCATCAATG GGAGCCAGGT
GTGGGCAGGA CAGCCAGTGT ATCCCCAGGA AACTGACGAT GCCTGCATCT TCCCTGATGG
TGGACCTTGC CCATCTGGCT CTTGGTCTCA GAAGAGAAGC TTTGTTTATG TCTGGAAGAC
CTGGGGCCAA TACTGGCAAG TTCTAGGGGG CCCAGTGTCT GGGCTGAGCA TTGGGACAGG
CAGGGCAATG CTGGGCACAC ACACGATGGA AGTGACTGTC TACCATCGCC GGGGATCCCG
GAGCTATGTG CCTCTTGCTC ATTCCAGCTC AGCCTTCACC ATTATGGACC AGGTGCCTTT
CTCCGTGAGC GTGTCCCAGT TGCGGGCCTT GGATGGAGGG AACAAGCACT TCCTGAGAAA
TCAGCCTCTG ACCTTTGCCC TCCAGCTCCA TGACCCCAGT GGCTATCTGG CTGAAGCTGA
CCTCTCCTAC ACCTGGGACT TTGGAGACAG TAGTGGAACC CTGATCTCTC GGGCACTTGT
GGTCACTCAT ACTTACCTGG AGCCTGGCCC AGTCACTGTT CAGGTGGTCC TGCAGGCTGC
CATTCCTCTC ACCTCCTGTG GCTCCTCCCC AGTTCCAGGC ACCACAGATG GGCACAGGCC
AACTGCAGAG GCCCCTAACA CCACAGCTGG CCAAGTGCCT ACTACAGAAG TTGTGGGTAC
TACACCTGGT CAGGCGCCAA CTGCAGAGCC CTCTGGAACC ACATCTGTGC AGGTGCCAAC
CACTGAAGTC ATAAGCACTG CACCTGTGCA GATGCCAACT GCAGAGAGCA CAGGTATGAC
ACCTGAGAAG GTGCCAGTTT CAGAGGTCAT GGGTACCACA CTGGCAGAGA TGTCAACTCC
AGAGGCTACA GGTATGACAC CTGCAGAGGT ATCAATTGTG GTGCTTTCTG GAACCACAGC
TGCACAGGTA ACAACTACAG AGTGGGTGGA GACCACAGCT AGAGAGCTAC CTATCCCTGA
GCCTGAAGGT CCAGATGCCA GCTCAATCAT GTCTACGGAA AGTATTACAG GTTCCCTGGG
CCCCCTGCTG GATGGTACAG CCACCTTAAG GCTGGTGAAG AGACAAGTCC CCCTGGATTG
TGTTCTGTAT CGATATGGTT CCTTTTCCGT CACCCTGGAC ATTGTCCAGG GTATTGAAAG
TGCCGAGATC CTGCAGGCTG TGCCGTCCGG TGAGGGGGAT GCATTTGAGC TGACTGTGTC
CTGCCAAGGC GGGCTGCCCA AGGAAGCCTG CATGGAGATC TCATCGCCAG GGTGCCAGCC
CCCTGCCCAG CGGCTGTGCC AGCCTGTGCT ACCCAGCCCA GCCTGCCAGC TGGTTCTGCA
CCAGATACTG AAGGGTGGCT CGGGGACATA CTGCCTCAAT GTGTCTCTGG CTGATACCAA
CAGCCTGGCA GTGGTCAGCA CCCAGCTTAT CATGCCTGGT CAAGAAGCAG GCCTTGGGCA
GGTTCCGCTG ATCGTGGGCA TCTTGCTGGT GTTGATGGCT GTGGTCCTTG CATCTCTGAT
ATATAGGCGC AGACTTATGA AGCAAGACTT CTCCGTACCC CAGTTGCCAC ATAGCAGCAG
TCACTGGCTG CGTCTACCCC GCATCTTCTG CTCTTGTCCC ATTGGTGAGA ACAGCCCCCT
CCTCAGTGGG CAGCAGGTCT GA
```

FIGURE 7

```
Met Asp Leu Val Leu Lys Arg Cys Leu Leu His Leu Ala Val Ile Gly
 1                5                  10                  15

Ala Leu Leu Ala Val Gly Ala Thr Lys Val Pro Arg Asn Gln Asp Trp
             20                  25                  30

Leu Gly Val Ser Arg Gln Leu Arg Thr Lys Ala Trp Asn Arg Gln Leu
         35                  40                  45

Tyr Pro Glu Trp Thr Glu Ala Gln Arg Leu Asp Cys Trp Arg Gly Gly
         50                  55                  60

Gln Val Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu Ile Gly Ala
65                  70                  75                  80

Asn Ala Ser Phe Ser Ile Ala Leu Asn Phe Pro Gly Ser Gln Lys Val
                 85                  90                  95

Leu Pro Asp Gly Gln Val Ile Trp Val Asn Asn Thr Ile Ile Asn Gly
             100                 105                 110

Ser Gln Val Trp Gly Gly Gln Pro Val Tyr Pro Gln Glu Thr Asp Asp
             115                 120                 125

Ala Cys Ile Phe Pro Asp Gly Gly Pro Cys Pro Ser Gly Ser Trp Ser
     130                 135                 140

Gln Lys Arg Ser Phe Val Tyr Val Trp Lys Thr Trp Gly Gln Tyr Trp
145                 150                 155                 160

Gln Val Leu Gly Gly Pro Val Ser Gly Leu Ser Ile Gly Thr Gly Arg
             165                 170                 175

Ala Met Leu Gly Thr His Thr Met Glu Val Thr Val Tyr His Arg Arg
             180                 185                 190

Gly Ser Arg Ser Tyr Val Pro Leu Ala His Ser Ser Ser Ala Phe Thr
         195                 200                 205

         Met
Ile Thr Asp Gln Val Pro Phe Ser Val Ser Val Ser Gln Leu Arg Ala
    210                 215                 220

Leu Asp Gly Gly Asn Lys His Phe Leu Arg Asn Gln Pro Leu Thr Phe
225                 230                 235                 240

Ala Leu Gln Leu His Asp Pro Ser Gly Tyr Leu Ala Glu Ala Asp Leu
             245                 250                 255

Ser Tyr Thr Trp Asp Phe Gly Asp Ser Ser Gly Thr Leu Ile Ser Arg
             260                 265                 270

                                                         Val
Ala Leu Val Val Thr His Thr Tyr Leu Glu Pro Gly Pro Val Thr Ala
         275                 280                 285

Gln Val Val Leu Gln Ala Ala Ile Pro Leu Thr Ser Cys Gly Ser Ser
         290                 295                 300

Pro Val Pro Gly Thr Thr Asp Gly His Arg Pro Thr Ala Glu Ala Pro
305                 310                 315                 320

Asn Thr Thr Ala Gly Gln Val Pro Thr Thr Glu Val Val Gly Thr Thr
             325                 330                 335

Pro Gly Gln Ala Pro Thr Ala Glu Pro Ser Gly Thr Thr Ser Val Gln
             340                 345                 350

Val Pro Thr Thr Glu Val Ile Ser Thr Ala Pro Val Gln Met Pro Thr
         355                 360                 365
```

FIGURE 7 (CONT'D)

```
Ala Glu Ser Thr Gly Met Thr Pro Glu Lys Val Pro Val Ser Glu Val
    370             375         380

Met Gly Thr Thr Leu Ala Glu Met Ser Thr Pro Glu Ala Thr Gly Met
385             390         395                 400

Thr Pro Ala Glu Val Ser Ile Val Val Leu Ser Gly Thr Thr Ala Ala
            405             410             415

Gln Val Thr Thr Thr Glu Trp Val Glu Thr Thr Ala Arg Glu Leu Pro
        420             425             430

Ile Pro Glu Pro Glu Gly Pro Asp Ala Ser Ser Ile Met Ser Thr Glu
        435         440             445

Ser Ile Thr Gly Ser Leu Gly Pro Leu Leu Asp Gly Thr Ala Thr Leu
    450             455             460

Arg Leu Val Lys Arg Gln Val Pro Leu Asp Cys Val Leu Tyr Arg Tyr
465             470             475             480

Gly Ser Phe Ser Val Thr Leu Asp Ile Val Gln Gly Ile Glu Ser Ala
            485             490             495

Glu Ile Leu Gln Ala Val Pro Ser Gly Glu Gly Asp Ala Phe Glu Leu
            500             505             510

Thr Val Ser Cys Gln Gly Gly Leu Pro Lys Glu Ala Cys Met Glu Ile
            515             520             525

Ser Ser Pro Gly Cys Gln Pro Pro Ala Gln Arg Leu Cys Gln Pro Val
    530             535             540

Leu Pro Ser Pro Ala Cys Gln Leu Val Leu His Gln Ile Leu Lys Gly
545             550             555             560

Gly Ser Gly Thr Tyr Cys Leu Asn Val Ser Leu Ala Asp Thr Asn Ser
            565             570             575

Leu Ala Val Val Ser Thr Gln Leu Ile Met Pro Gly Gln Glu Ala Gly
            580             585             590

Leu Gly Gln Val Pro Leu Ile Val Gly Ile Leu Leu Val Leu Met Ala
        595             600             605

Val Val Leu Ala Ser Leu Ile Tyr Arg Arg Arg Leu Met Lys Gln Asp
    610             615             620

Phe Ser Val Pro Gln Leu Pro His Ser Ser Ser His Trp Leu Arg Leu
625             630             635             640

Pro Arg Ile Phe Cys Ser Cys Pro Ile Gly Glu Asn Ser Pro Leu Leu
            645             650             655

Ser Gly Gln Gln Val
            660
```

ATGGAGTCTCCCTCGGCCCCCCCCCACAGATGGTGCATCCCCTGGCAGAGGCTCCTGCT
```
  1 ---------+---------+---------+---------+---------+---------+  60
```
TACCTCAGAGGGAGCCGGGGAGGGGTGTCTACCACGTAGGGGACCGTCTCCGAGGACGAG

a   M   E   S   P   S   A   P   P   H   R   W   C   I   P   W   Q   R   L   L   L   -

ACAGCCTCACTTCTAACCTTCTGGAACCCGCCCACCACTGCCAAGCTCACTATTGAATCC
```
 61 ---------+---------+---------+---------+---------+---------+ 120
```
TGTCGGAGTGAAGATTGGAAGACCTTGGGCGGGTGGTGACGGTTCGAGTGATAACTTAGG

a   T   A   S   L   L   T   F   W   N   P   P   T   T   A   K   L   T   I   E   S   -

ACGCCGTTCAATGTCGCAGAGGGGAAGGAGGTGCTTCTACTTGTCCACAATCTGCCCCAG
```
121 ---------+---------+---------+---------+---------+---------+ 180
```
TGCGGCAAGTTACAGCGTCTCCCCTTCCTCCACGAAGATGAACAGGTGTTAGACGGGGTC

a   T   P   F   N   V   A   E   G   K   E   V   L   L   L   V   H   N   L   P   Q   -

CATCTTTTTGGCTACAGCTGGTACAAAGGTGAAAGAGTGGATGGCAACCGTCAAATTATA
```
181 ---------+---------+---------+---------+---------+---------+ 240
```
GTAGAAAAACCGATGTCGACCATGTTTCCACTTTCTCACCTACCGTTGGCAGTTTAATAT

a   H   L   F   G   Y   S   W   Y   K   G   E   R   V   D   G   N   R   Q   I   I   -

GGATATGTAATAGGAACTCAACAAGCTACCCCAGGGCCCGCATACAGTGGTCGAGAGATA
```
241 ---------+---------+---------+---------+---------+---------+ 300
```
CCTATACATTATCCTTGAGTTGTTCGATGGGGTCCCGGGCGTATGTCACCAGCTCTCTAT

a   G   Y   V   I   G   T   Q   Q   A   T   P   G   P   A   Y   S   G   R   E   I   -

ATATACCCCAATGCATCCCTGCTGATCCAGAACATCATCCAGAATGACACAGGATTCTAC
```
301 ---------+---------+---------+---------+---------+---------+ 360
```
TATATGGGGTTACGTAGGGACGACTAGGTCTTGTAGTAGGTCTTACTGTGTCCTAAGATG

a   I   Y   P   N   A   S   L   L   I   Q   N   I   I   Q   N   D   T   G   F   Y   -

ACCCTACACGTCATAAAGTCAGATCTTGTGAATGAAGAAGCAACTGGCCAGTTCCGGGTA
```
361 ---------+---------+---------+---------+---------+---------+ 420
```
TGGGATGTGCAGTATTTCAGTCTAGAACACTTACTTCTTCGTTGACCGGTCAAGGCCCAT

a   T   L   H   V   I   K   S   D   L   V   N   E   E   A   T   G   Q   F   R   V   -

TACCCGGAGCTGCCCAAGCCCTCCATCTCCAGCAACAACTCCAAACCCGTGGAGGACAAG
```
421 ---------+---------+---------+---------+---------+---------+ 480
```
ATGGGCCTCGACGGGTTCGGGAGGTAGAGGTCGTTGTTGAGGTTTGGGCACCTCCTGTTC

a   Y   P   E   L   P   K   P   S   I   S   S   N   N   S   K   P   V   E   D   K   -

GATGCTGTGGCCTTCACCTGTGAACCTGAGACTCAGGACGCAACCTACCTGTGGTGGGTA
```
481 ---------+---------+---------+---------+---------+---------+ 540
```
CTACGACACCGGAAGTGGACACTTGGACTCTGAGTCCTGCGTTGGATGGACACCACCCAT

a   D   A   V   A   F   T   C   E   P   E   T   Q   D   A   T   Y   L   W   W   V   -

AACAATCAGAGCCTCCCGGTCAGTCCCAGGCTGCAGCTGTCCAATGGCAACAGGACCCTC
```
541 ---------+---------+---------+---------+---------+---------+ 600
```
TTGTTAGTCTCGGAGGGCCAGTCAGGGTCCGACGTCGACAGGTTACCGTTGTCCTGGGAG

a   N   N   Q   S   L   P   V   S   P   R   L   Q   L   S   N   G   N   R   T   L   -

ACTCTATTCAATGTCACAAGAAATGACACAGCAAGCTACAAATGTGAAACCCAGAACCCA
```
601 ---------+---------+---------+---------+---------+---------+ 660
```
TGAGATAAGTTACAGTGTTCTTTACTGTGTCGTTCGATGTTTACACTTTGGGTCTTGGGT

a   T   L   F   N   V   T   R   N   D   T   A   S   Y   K   C   E   T   Q   N   P   -

GTGAGTGCCAGGCGCAGTGATTCAGTCATCCTGAATGTCCTCTATGGCCCGGATGCCCCC
```
661 ---------+---------+---------+---------+---------+---------+ 720
```
CACTCACGGTCCGCGTCACTAAGTCAGTAGGACTTACAGGAGATACCGGGCCTACGGGGG

a   V   S   A   R   R   S   D   S   V   I   L   N   V   L   Y   G   P   D   A   P   -

Figure 8

```
        ACCATTTCCCCTCTAAA●    CTTACAGATCAGGGGAAAATCTGAACCTCTCCTGCC●
    721 ---------+---------+---------+---------+---------+---------+ 780
        TGGTAAAGGGGAGATTTGTGTAGAATGTCTAGTCCCCTTTTAGACTTGGAGAGGACGGTG

 a      T  I  S  P  L  N  T  S  Y  R  S  G  E  N  L  N  L  S  C  H  -

        GCAGCCTCTAACCCACCTGCACAGTACTCTTGGTTTGTCAATGGGACTTTCCAGCAATCC
    781 ---------+---------+---------+---------+---------+---------+ 840
        CGTCGGAGATTGGGTGGACGTGTCATGAGAACCAAACAGTTACCCTGAAAGGTCGTTAGG

 a      A  A  S  N  P  P  A  Q  Y  S  W  F  V  N  G  T  F  Q  Q  S  -

        ACCCAAGAGCTCTTTATCCCCAACATCACTGTGAATAATAGTGGATCCTATACGTGCCAA
    841 ---------+---------+---------+---------+---------+---------+ 900
        TGGGTTCTCGAGAAATAGGGGTTGTAGTGACACTTATTATCACCTAGGATATGCACGGTT

 a      T  Q  E  L  F  I  P  N  I  T  V  N  N  S  G  S  Y  T  C  Q  -

        GCCCATAACTCAGACACTGGCCTCAATAGGACCACAGTCACGACGATCACAGTCTATGAG
    901 ---------+---------+---------+---------+---------+---------+ 960
        CGGGTATTGAGTCTGTGACCGGAGTTATCCTGGTGTCAGTGCTGCTAGTGTCAGATACTC

 a      A  H  N  S  D  T  G  L  N  R  T  T  V  T  T  I  T  V  Y  E  -

        CCACCCAAACCCTTCATCACCAGCAACAACTCCAACCCCGTGGAGGATGAGGATGCTGTA
    961 ---------+---------+---------+---------+---------+---------+ 1020
        GGTGGGTTTGGGAAGTAGTGGTCGTTGTTGAGGTTGGGGCACCTCCTACTCCTACGACAT

 a      P  P  K  P  F  I  T  S  N  N  S  N  P  V  E  D  E  D  A  V  -

        GCCTTAACCTGTGAACCTGAGATTCAGAACACAACCTACCTGTGGTGGGTAAATAATCAG
   1021 ---------+---------+---------+---------+---------+---------+ 1080
        CGGAATTGGACACTTGGACTCTAAGTCTTGTGTTGGATGGACACCACCCATTTATTAGTC

 a      A  L  T  C  E  P  E  I  Q  N  T  T  Y  L  W  W  V  N  N  Q  -

        AGCCTCCCGGTCAGTCCCAGGCTGCAGCTGTCCAATGACAACAGGACCCTCACTCTACTC
   1081 ---------+---------+---------+---------+---------+---------+ 1140
        TCGGAGGGCCAGTCAGGGTCCGACGTCGACAGGTTACTGTTGTCCTGGGAGTGAGATGAG

 a      S  L  P  V  S  P  R  L  Q  L  S  N  D  N  R  T  L  T  L  L  -

        AGTGTCACAAGGAATGATGTAGGACCCTATGAGTGTGGAATCCAGAACGAATTAAGTGTT
   1141 ---------+---------+---------+---------+---------+---------+ 1200
        TCACAGTGTTCCTTACTACATCCTGGGATACTCACACCTTAGGTCTTGCTTAATTCACAA

 a      S  V  T  R  N  D  V  G  P  Y  E  C  G  I  Q  N  E  L  S  V  -

        GACCACAGCGACCCAGTCATCCTGAATGTCCTCTATGGCCCAGACGACCCCACCATTTCC
   1201 ---------+---------+---------+---------+---------+---------+ 1260
        CTGGTGTCGCTGGGTCAGTAGGACTTACAGGAGATACCGGGTCTGCTGGGGTGGTAAAGG

 a      D  H  S  D  P  V  I  L  N  V  L  Y  G  P  D  D  P  T  I  S  -

        CCCTCATACACCTATTACCGTCCAGGGGTGAACCTCAGCCTCTCCTGCCATGCAGCCTCT
   1261 ---------+---------+---------+---------+---------+---------+ 1320
        GGGAGTATGTGGATAATGGCAGGTCCCCACTTGGAGTCGGAGAGGACGGTACGTCGGAGA

 a      P  S  Y  T  Y  Y  R  P  G  V  N  L  S  L  S  C  H  A  A  S  -

        AACCCACCTGCACAGTATTCTTGGCTGATTGATGGGAACATCCAGCAACACACACAAGAG
   1321 ---------+---------+---------+---------+---------+---------+ 1380
        TTGGGTGGACGTGTCATAAGAACCGACTAACTACCCTTGTAGGTCGTTGTGTGTGTTCTC

 a      N  P  P  A  Q  Y  S  W  L  I  D  G  N  I  Q  Q  H  T  Q  E  -

        CTCTTTATCTCCAACATCACTGAGAAGAACAGCGGACTCTATACCTGCCAGGCCAATAAC
   1381 ---------+---------+---------+---------+---------+---------+ 1440
        GAGAAATAGAGGTTGTAGTGACTCTTCTTGTCGCCTGAGATATGGACGGTCCGGTTATTG

 a      L  F  I  S  N  I  T  E  K  N  S  G  L  Y  T  C  Q  A  N  N  -
```

Figure 8, con't

```
            TCAGCCAGTGGCCACAC   ●  ACTACAGTCAAGACAATCACAGTCTCTGCGGAGCTGC ●
      1441  ---------+------  ●  --------+---------+---------+-------  ● 500
            AGTCGGTCACCGGTGTCGTCCTGATGTCAGTTCTGTTAGTGTCAGAGACGCCTCGACGGG

      a      S   A   S   G   H   S   R   T   T   V   K   T   I   T   V   S   A   E   L   P   -

            AAGCCCTCCATCTCCAGCAACAACTCCAAACCCGTGGAGGACAAGGATGCTGTGGCCTTC
      1501  ---------+---------+---------+---------+---------+---------+ 1560
            TTCGGGAGGTAGAGGTCGTTGTTGAGGTTTGGGCACCTCCTGTTCCTACGACACCGGAAG

      a      K   P   S   I   S   S   N   N   S   K   P   V   E   D   K   D   A   V   A   F   -

            ACCTGTGAACCTGAGGCTCAGAACACAACCTACCTGTGGTGGGTAAATGGTCAGAGCCTC
      1561  ---------+---------+---------+---------+---------+---------+ 1620
            TGGACACTTGGACTCCGAGTCTTGTGTTGGATGGACACCACCCATTTACCAGTCTCGGAG

      a      T   C   E   P   E   A   Q   N   T   T   Y   L   W   W   V   N   G   Q   S   L   -

            CCAGTCAGTCCCAGGCTGCAGCTGTCCAATGGCAACAGGACCCTCACTCTATTCAATGTC
      1621  ---------+---------+---------+---------+---------+---------+ 1680
            GGTCAGTCAGGGTCCGACGTCGACAGGTTACCGTTGTCCTGGGAGTGAGATAAGTTACAG

      a      P   V   S   P   R   L   Q   L   S   N   G   N   R   T   L   T   L   F   N   V   -

            ACAAGAAATGACGCAAGAGCCTATGTATGTGGAATCCAGAACTCAGTGAGTGCAAACCGC
      1681  ---------+---------+---------+---------+---------+---------+ 1740
            TGTTCTTTACTGCGTTCTCGGATACATACACCTTAGGTCTTGAGTCACTCACGTTTGGCG

      a      T   R   N   D   A   R   A   Y   V   C   G   I   Q   N   S   V   S   A   N   R   -

            AGTGACCCAGTCACCCTGGATGTCCTCTATGGGCCGGACACCCCCATCATTTCCCCCCCA
      1741  ---------+---------+---------+---------+---------+---------+ 1800
            TCACTGGGTCAGTGGGACCTACAGGAGATACCCGGCCTGTGGGGGTAGTAAAGGGGGGGT

      a      S   D   P   V   T   L   D   V   L   Y   G   P   D   T   P   I   I   S   P   P   -

            GACTCGTCTTACCTTTCGGGAGCGGACCTCAACCTCTCCTGCCACTCGGCCTCTAACCCA
      1801  ---------+---------+---------+---------+---------+---------+ 1860
            CTGAGCAGAATGGAAAGCCCTCGCCTGGAGTTGGAGAGGACGGTGAGCCGGAGATTGGGT

      a      D   S   S   Y̲   L̲   S̲   G̲   A̲   D̲   L̲   N̲   L̲   S   C   H   S   A   S   N   P   -

            TCCCCGCAGTATTCTTGGCGTATCAATGGGATACCGCAGCAACACACACAAGTTCTCTTT
      1861  ---------+---------+---------+---------+---------+---------+ 1920
            AGGGGCGTCATAAGAACCGCATAGTTACCCTATGGCGTCGTTGTGTGTGTTCAAGAGAAA

      a      S   P   Q   Y   S   W   R   I   N   G   I   P   Q   Q   H   T   Q   V   L   F   -

            ATCGCCAAAATCACGCCAAATAATAACGGGACCTATGCCTGTTTTGTCTCTAACTTGGCT
      1921  ---------+---------+---------+---------+---------+---------+ 1980
            TAGCGGTTTTAGTGCGGTTTATTATTGCCCTGGATACGGACAAAACAGAGATTGAACCGA

      a      I   A   K   I   T   P   N   N   N   G   T   Y   A   C   F   V   S   N   L   A   -

            ACTGGCCGCAATAATTCCATAGTCAAGAGCATCACAGTCTCTGCATCTGGAACTTCTCCT
      1981  ---------+---------+---------+---------+---------+---------+ 2040
            TGACCGGCGTTATTAAGGTATCAGTTCTCGTAGTGTCAGAGACGTAGACCTTGAAGAGGA

      a      T   G   R   N   N   S   I   V   K   S   I   T   V   S   A   S   G   T   S   P   -

            GGTCTCTCAGCTGGGGCCACTGTCGGCATCATGATTGGAGTGCTGGTTGGGGTTGCTCTG
      2041  ---------+---------+---------+---------+---------+---------+ 2100
            CCAGAGAGTCGACCCCGGTGACAGCCGTAGTACTAACCTCACGACCAACCCCAACGAGAC

      a      G   L   S   A   G   A   T   V   G   I   M   I   G   V   L   V   G   V   A   L   -

            ATATAG  ◄─
      2101  ------ 2106
            TATATC

      a      I   * ◄─
```

Figure 8, con't